Claims

1. A method for determining the identity of one or more mutations or single nucleotide polymorphisms (SNPs) in a genome, comprising:

a. contacting a sample genome, under conditions which permit template dependant oligonucleotide ligation, with a plurality of different oligonucleotide molecules which comprise

(i) a first set of oligonucleotides each comprising a sequence of nucleotides that is complementary to a region on said genome that includes a known SNP site and which oligonucleotides are complementary to said region other than at a base at or near the 5' end of said oligonucleotides that is to be tested for complementarity to a base at the SNP site, each of said oligonucleotides comprising a unique label to identify both the base to be tested and the position of the SNP to be scored,

(ii) a second set of oligonucleotides each comprising a sequence of nucleotides complementary to a region on said target genome for hybridisation with said target genome adjacent the 5' end of an oligonucleotide of said first oligonucleotide set, and a surface capture moiety,

a phosphate moiety being located at any of either the 5' end of said first set of oligonucleotides or the 3' end of said second set of oligonucleotides,

any resulting ligated oligonucleotide being immobilised on a solid support via the surface capture moiety,

b. analysing said solid support for the identity of one or more of said unique labels and comparing the defined bases in any of said immobilised oligonucleotides to those of the reference one or more SNPs.

2. A method according to claim 1, wherein in step (a) each of said oligonucleotides in said first oligonucleotide set includes one of any of the defined nucleotide bases A, C, T or G for testing for complementarity with said SNP.

3. A method according to claim 1 or 2 wherein said first oligonucleotide includes a sequence of nucleotides complementary to the target genome up to but not including the

SNP site, the base to be tested for complementarity being located at the 5' end of each of said oligonucleotides in said first oligonucleotide set.

4. A method according to any of claims 1 to 3, wherein each of the oligonucleotides of said first oligonucleotide set includes a hairpin oligonucleotide.

5. A method according to any of claims 1 to 4 wherein said label is a unique coding sequence of nucleotides in said first oligonucleotide set.

6. A method according to claim 5 that further comprises the steps of carrying out the sequencing reaction(s) and detecting the incorporation of bases into the immobilised oligonucleotide to determine at least the unique coding sequence.

7. A method according to any of claims 1 to 6 wherein said oligonucleotides are immobilised on said support at a density that allows each immobilised oligonucleotide to be individually resolved by optical microscopy.

8. A method according to any preceding claim wherein the ligated product of said first and second sets of oligonucleotides comprises between 10 and 70 bases.

9. A method according to any preceding claim wherein the ligated product of said first and second sets of oligonucleotide comprises from 30 to 50 bases.

10. A method according to any preceding claim, wherein said method is performed for a plurality of SNPs.

11. A method according to any preceding claim wherein said sample genomic DNA is fragmented prior to contacting with said sets of oligonucleotides.

12. A method according to any preceding claim, wherein said oligonucleotides are contacted with said genome in the presence of a DNA ligase.

13. A method according to any of claims 1 to 11, wherein said first and second sets of oligonucleotides are contacted with said genome under conditions that permit non-enzymatic chemical ligation.

14. A method according to claim 13, wherein said oligonucleotides are contacted with 5'-iodide and 3'-selenophosphate.